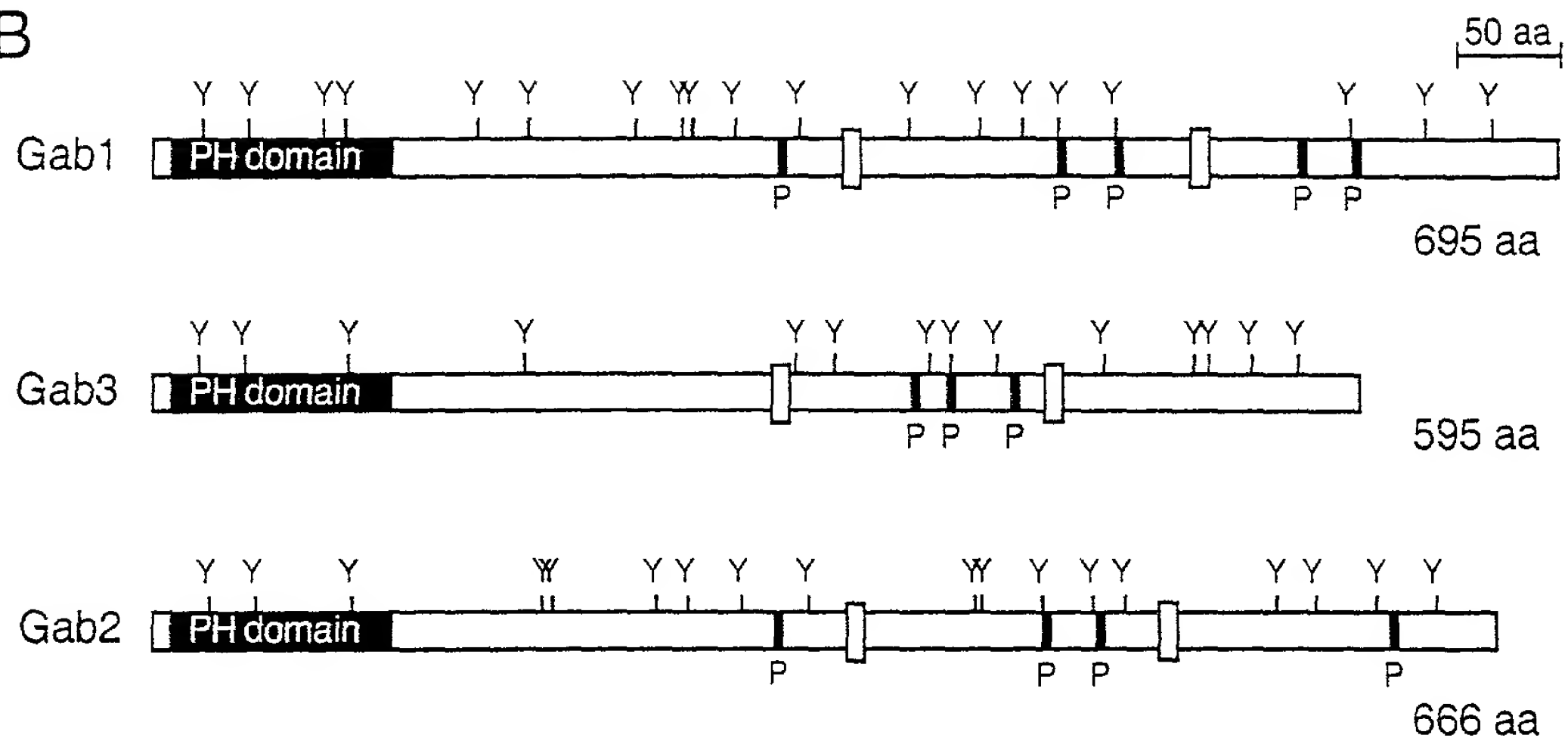


A

Human	MSAGDAVCTGWLVKSPPERKLQRYAWRKRWFVLRGRMSGNPDVLEYRKNHSSKPIRVI	60
Murine	MSTGDTVCMGWLIKSPPERKLQRYAWRKRWFVLRGRMSGNPDVLEYRKNHSNKPIRVI	60
	:*:*:* *:*****.*****	
Human	DLSECAVWKHVGPSFVRKEFQNNFVFIVKTTSRTFYLVAKTEQEMQVWVHSISQVCN LGH	120
Murine	DLSECTVWKHAGPGFIRKEFQKNFVFIVKTTSRTFYLVAKTEEEMQVWVHSISQVCN FSH	120
	*****:*****.*:*:*****:*****:*****:*****:.*	
Human	LEDGADSMESLSYTPSSLQPSSASSLLTAHAASSSLPRDDPNTNAVATEETRSESELLFL	180
Murine	LEDGADSMESLSHMPSSFQPSPASSLHTVHVANSALLKDDGNTNSVVTEETRRESEFLFL	180
	*****:*****:*****.*.*.*:*:* ***:***** ***:***	
Human	PDYLVLSNCETGRLHHTSLPTRCDSWSNSDRSLEQASFDDVFVDCLQPLPSSHLVHPSCH	240
Murine	PDYLILSNCETGRLHHASLPTRCDSWSNSNHS LAQTSFDDVF LDGLQPFISNNLVHPLHH	240
	****:*****:*****:*** *:*:*****:* ***: *.:***** *	
Human	GSGAQEVPSSRPQAALIWSREINGPPRDHLSSSPLESLSSTIQVDKNQGS LPCGAKEL	300
Murine	GKVSQDFPSIRPQASLIWNREINGPSRNLMS SPLES LNPTVHVEEKQVSLPSGVKEL	300
	.::.* ***:*****.*: :*****.*.:*:*:.* ***.*.***	
Human	DIMSNTPPPRPPKPSHLSERRQEE--WSTHSGSKKPECTLVPRRISLSGLDNMRTWKADV	358
Murine	NIMSNIPPPRPPKPSYLSEQRQDQPLLTGHSSNKKPGYTMVPRRISLSGLDHVGSWKGDV	360
	:**** *****:***:***: : **..*** *:*****: : **.*	
Human	EGQSLRHRDKRLSLNLPCRFS <u>PMYPT</u> ASASIEDSYV <u>PMSE</u> <u>QAGASGLGPHCSPDDYIPMN</u>	418
Murine	QSQSLRHRDKRLSLNLPCKFSP <u>PIYPT</u> ASPSAEDSYV <u>PMSE</u> <u>PKGTASELRPHCSQDDYIPMS</u>	420
	:..*****:***:*****.* *****:.. ** * **** *****.	
Human	SGSISSPLPELPANLEPPPVNRDLKPQRKSRPPPLDLRNLSIIREHASLTRTRTVPCSR	478
Murine	S----SMLPELPADLEPPPVNRNLKPQRKSRPPPLDSRNLSITIQEHTSLTRTYTVPCNRT	476
	* * *****:*****:***** ***** *:***:***** *****.*	
Human	SFLSPERNGIN SARFFANPV <u>SREDEES</u> ----- <u>YIEME</u> EHRTASSLS SGALTWTK	527
Murine	SFLSPQRNGINCARLFSTPSEEEEEEEEEEEEEEEKYIQMEEYGT VSSLSRSALSWTK	536
	*****:*****.*:*:.* ..*:**.* ***:***: *.***** ***:***	
Human	<u>SHP2</u> KFSLDYLALDFNSASPAPMQKLLLSEEQRVDYVQVDEQKTQALQSTKQEWTDERQSKV	586
Murine	<u>SHP2</u> KFSLDYLALDFNSTSPAPVQKLLLSEEQRVDYVQVDEQKTQAFRSTKQAWTDERQSKV	595
	*****:*****:*:*****:*****:*****:***** *****	

Figure 1A

[illegible]

C

Gab3	MSTG--D-TVCMGWLIKSPPERKLQRYAWRKRWFLRRGR	37
Gab2	MSGGGGDDVCTGWLRKSPPEKKLRRYAWKKRWFILRSGR	40
Gab1	MSGG--E-VVCSGWLRKSPPEKKLKRYAWKRRWFLRSGR	37
	** * : . ** *** *****: ** : *****: : *****: ** **	
Gab3	MSGNPDVLEYRKNKHSNKPIRVIDLSECTVWKHAGPGFIR	77
Gab2	MSGDPDVLEYKNEHSHKPLRIINLNLCEQVD-AGLTFNK	79
Gab1	LTGDPDVLEYKNDHAKKPIRIIDLNLCCQVD-AGLTFNK	76
	: : * : ***** : * . * : : ** : * : * : * . * . ** * :	
Gab3	KEFQKNFVFIKTTSRIFYLVAKTEEEMQVWVHSISQVCN	117
Gab2	KELQDSFVFDIKTSERTIFYLVAETeadmNKWVQSICQICG	119
Gab1	KEFENSYIFDINTIDRIFYLVADSEEDMKNKWVRCICDICG	116
	** : : . . : : * : : * . * ***** . : * : * : ** : . * . : : * .	

Figure 1B and C